

SEQUENCE LISTING

| <110> | Scheiflinger, Friedrich Kerschbaumer, Randolf Falkner, Falko-Guenter Dorner, Friedrich Baxter Aktiengesellschaft | |
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| <120> | Factor IX/Factor IXa Activating Antibodies and Antibody Derivatives | |
| <130> | 20695C-005900US | |
| | US 09/661,992 2000-09-14 | |
| | AT A157600 1999-09-14 | |
| <160> | 112 | |
| <170> | PatentIn Ver. 2.1 | |
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| \ _ 13> | Michiela boquono | |
| <220> | | |
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| <213> <220> <223> <400> ggccgccatc | DNA Artificial Sequence Description of Artificial Sequence:oligonucleotide mychis6-co 79 cagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca actaa taag | 60 74 |
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| <213> <220> <223> <400> ggccgccatc. <210> <211> | DNA Artificial Sequence Description of Artificial Sequence:oligonucleotide mychis6-co 79 cagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca actaa taag 80 74 | 60 74 |
| <213> <220> <223> <400> ggccgccatc. <210> <211> <212> | DNA Artificial Sequence Description of Artificial Sequence:oligonucleotide mychis6-co 79 cagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca actaa taag 80 74 DNA | 60 74 |
| <213> <220> <223> <400> ggccgccatc. <210> <211> <212> | DNA Artificial Sequence Description of Artificial Sequence:oligonucleotide mychis6-co 79 cagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca actaa taag 80 74 | 6074 |
| <213> <220> <223> <400> ggccgccatcd <210> <211> <212> <213> | DNA Artificial Sequence Description of Artificial Sequence:oligonucleotide mychis6-co 79 cagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca actaa taag 80 74 DNA | 60 74 |
| <213> <220> <223> <400> ggccgccatc. <210> <211> <212> <213> | DNA Artificial Sequence Description of Artificial Sequence:oligonucleotide mychis6-co 79 cagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca actaa taag 80 74 DNA | 6074 |

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<400> 80
aattettatt agtgatggtg atggtgatgt geegeeceat teagateete ttetgagatg 60
agtttttgtt ctgc
<210> 81
<211> 726
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:scFv from
     hybridoma cell line 193/AD3
<400> 81
gaggtgaagc tggtggagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60
teetgeaagg ettetgggta tatetteaca aactatggaa tgaactgggt gaageagget 120
ccaggaaagg gtttaaagtg gatgggctgg ataaacacct acactggaga gccaacatat 180
gctgatgact tcaagggacg gtttgccttc tctttggaaa cctctgccag cactgcctat 240
ttgcagatca acaacctcaa aaatgaggac acggctacat atttctgtgc attatatggt 300
aactccccta aggggtttgc ttactggggc caagggactc tggtcactgt ctctgcaggt 360
ggaggcggtt caggtgggcg cgcctctggc ggtggcggat cggatattca gatgacacag 420
tctcccaaat tcctgcttgt atcagcagga gacagggtta ccataacctg caaggccagt 480
cagagtgtga gtaatgatgt agcttggtac caacagaagc cggggcagtc tcctaaacta 540
ctgatgtact atgcatccaa tcgctacact ggagtccctg atcgcttcac tggcagtgga 600
tatgggacgg atttcacttt caccatcagc actgtgcagg ctgaagacct ggcagtttat 660
ttctgtcagc aggattatgg ctctcctccc acgttcggag ggggcaccaa gctggaaatt 720
aaacgg
<210> 82
<211> 242
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:scFv from
      hybridoma cell line 193/AD3
<400> 82
Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
             20
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
                                              60
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly
                                105
            100
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Thr Leu Val Thr Val Ser Ala Gly Gly Gly Ser Gly Gly Arg Ala 115 Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe 135 140 Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser 145 Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln 170 165 Ser Pro Lys Leu Leu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val 185 180 Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr 200 Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln 215 210 Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile 235 230 Lys Arg <210> 83 <211> 747 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:scFv from hybridoma cell line 193/K2 <400> 83 gaagtgcagc tggtggagtc tgggggaggc ctagtgaagc ctggagggtc cctgaaactc 60 tcctgtgcag cctctggatt cactttcagt acctatacca tgtcttgggt tcgccagact 120 ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagtta cacctactat 180 ccagacagtg tgaggggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240 ctgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtac aagagatggg 300 ggacacgggt acggtagtag ctttgactac tggggccaag gcaccactct cacagtctcc 360 tcaggtggag gcggttcagg tgggcgcgcc tctggcggtg gcggatcgca aattgtgctc 420 acccagtete caeteteect geetgteagt ettggagate aageeteeat etettgeaga 480 tctagtcaga gcattgtaca tagtaatgga aacacctatt tagaatggta cctgcagaaa 540 ccaggccagt ctccaaagct cctgatctac aaagtttcca accgattttc tggggtccca 600 gacaaattca gtggcagtgg atcagggaca gatttcacac tcaagatcag cagagtggag 660 gctgaggatc tgggagttta ttactgcttt caaggttcac atgttccgtg gacgttcggt 720 ggaggcacca agctggaaat caaacgg <210> 84 <211> 249 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence:scFv from hybridoma cell line 193/K2

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val 35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro 130 135 140

Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp 165 170 175

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val 180 185 190

Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser Gly Ser 195 200 205

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu 210 215 220

Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly 225 230 235 240

Gly Gly Thr Lys Leu Glu Ile Lys Arg 245

<210> 85

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:scFv from hybridoma cell line 198/AB2 (subclone of 198/B1)

<400> 85

gaggtgcagc ttcaggagtc agggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tectgtgcag cetetggatt caettteagt agetatacea tgtettgggt tegecagaet 120 ceggagaaga ggetggagtg ggtegeaace attagtagtg gtggtagtte caectactat 180 ceagacagtg tgaagggeeg atteaceate tecagagaea atgecaagaa caecetgtae 240 ctgeaaatga geagtetgag gtetgaggae acageeatgt attactgtae aagagagggg 300 ggtggtttea cegteaactg gtaettegat gtetggggeg eagggaetet ggteaactgt 360 tetgeaggtg gaggeggte aggtgggee geetetggeg gtggeggate ggaaaatgtg 420 cteaceeagt etecagette tttggetgtg tetetaggge agagggeeae catateetge 480 caggacage aaagtgttga tagttatgge tataatttta tgeaetggta teggaatee 540 ceagggtea gtggeagtg gtetaggaea gaetteaee teaceattaa teetgtggag 660 getgatgatg ttgeaaceta ttaetgteag caaagtaatg agateeget caegtteggt 720 aetgggacea gaettggaaaat aaaaegg

<210> 86

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:scFv from hybridoma cell line 198/AB2 (subclone of 198/B1)

<400> 86

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys 85 90 95

Thr Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp 100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly 115 120 125

Gly Arg Ala Ser Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser 130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys 145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp 165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala 180 185 190

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Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
        195
Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
                        215
                                            220
Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
                    230
                                        235
Thr Gly Thr Arg Leu Glu Ile Lys Arg
                245
<210> 87
<211> 747
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:scFv derived
      from hybridima cell line 198/A1
<220>
<221> modified_base
<222> (1)..(747)
<223> n = g, a, c or t
<400> 87
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tcctgtgcag cctctggatt catttttagt agttatacca tgtcttgggt tcgccagact 120
ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagttc cacctactat 180
ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240
ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcactgtac aagagagggg 300
ggtggttatt acgtcaactg gtacttcgat gtctggggcg caggcaccac tctcacagtc 360
tectcaggtg gaggeggtte aggtgggege geetetggeg gtggeggate ggacattgag 420
ctcacncagt ctccagcttc tttggctgtg tctctagggc agagggccac catatcctgc 480
agagccagtg aaagtgttga tagttatggc aagagtttta tgcactggta ccagcagaaa 540
ccagggcagc cacccaaact cctcatctat cgtgcatcca acctagaatc tgggatccct 600
gccaggttca gtggcagtgg gtctaggaca gacttcaccc tcaccattaa tcctgtggag 660
gctgatgatg ttgcnaccta ttactgtcag caaagtaatg aggatcccct cacgttcggt 720
gctgggacca gactggaaat aaaacgg
<210> 88
<211> 249
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:scFv derived
      from hybridima cell line 198/A1
<400> 88
Glu Val Gln Leu Gln Glu Ser Gly Gly Leu Val Lys Pro Gly Gly
                                                          15
                  5
                                     10
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
                             40
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Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr 70 75 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys Thr Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly 115 120 Gly Arg Ala Ser Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser 135 Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp 170 Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala 185 Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser 200 195 Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val 215 Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly 225 230 235 Ala Gly Thr Arg Leu Glu Ile Lys Arg 245 <210> 89 <211> 2199 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence:198A2 scFv-alkaline phosphatase fusion protein (ORF of expression vector pDAP2-198AB2#100) <220>

<221> modified_base <222> (228) <223> n = g, a, c or t

<400> 89 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60 atggcggagg tgaagctggt ggagtctggg ggaggcttag tgaagcctgg agggtccctg 120 aaactctcct gtgcagcctc tggattcact ttcagtagct ataccatgtc ttgggttcgc 180 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtagtggngg tagttccacc 240 tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc 300

ctqtacctqc aaatgagcag tctgaggtct gaggacacag ccatgtatta ctgtacaaga 360 gagggggtg gtttcaccgt caactggtac ttcgatgtct ggggcgcagg aacctcagtc 420 acceptetect caggtggagg eggtteaggt gggegegeet etggeggtgg eggateggae 480 attgtgctga cacagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccata 540 tcctgcagag ccagtgaaag tgttgatagt tatggctata attttatgca ctggtatcag 600 cagataccag gacagecace caaacteete atetategtg catecaacet agagtetggg 660 atccctgcca ggttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct 720 gtggaggctg atgatgttgc aacctattac tgtcagcaaa gtaatgagga tccgctcacg 780 ttcggtactg ggaccagact ggaaataaaa cgggcggccg cagcccgggc accagaaatg 840 cctgttctgg aaaaccgggc tgctcagggc gatattactg cacccggcgg tgctcgccgt 900 ttaacqqqtq atcaqactqc cqctctqcqt gattctctta gcgataaacc tgcaaaaaat 960 attattttgc tgattggcga tgggatgggg gactcggaaa ttactgccgc acgtaattat 1020 gccgaaggtg cgggcgctt ttttaaaggt atagatgcct taccgcttac cgggcaatac 1080 actcactatg cgctgaataa aaaaaccggc aaaccggact acgtcaccga ctcggctgca 1140 tcagcaaccg cctggtcaac cggtgtcaaa acctataacg gcgcgctggg cgtcgatatt 1200 cacgaaaaag atcacccaac gattctggaa atggcaaaag ccgcaggtct ggcgaccggt 1260 aacgtttcta ccgcagagtt gcaggatgcc acgcccgctg cgctggtggc acatgtgacc 1320 tcgcgcaaat gctacggtcc gagcgcgacc agtgaaaaat gtccgggtaa cgctctggaa 1380 aaaggcggaa aaggatcgat taccgaacag ctgcttaacg ctcgtgccga cgttacgctt 1440 ggcggcggcg caaaaacctt tgctgaaacg gcaaccgctg gtgaatggca gggaaaaacg 1500 ctgcgtgaac aggcacaggc gcgtggttat cagttggtga gcgatgctgc ctcactgaat 1560 teggtgacgg aagcgaatca gcaaaaaccc etgettggce tgtttgetga eggcaatatg 1620 ccagtgcgct ggctaggacc gaaagcaacg taccatggca atatcgataa gcccgcagtc 1680 acctgtacgc caaatccgca acgtaatgac agtgtaccaa ccctggcgca gatgaccgac 1740 aaagccattg aattgttgag taaaaatgag aaaggctttt tcctgcaagt tgaaggtgcg 1800 tcaatcgata aacaggatca tgctgcgaat ccttgtgggc aaattggcga gacggtcgat 1860 ctcgatgaag ccgtacaacg ggcgctggaa ttcgctaaaa aggagggtaa cacgctggtc 1920 atagtcaccg ctgatcacgc ccacgccagc cagattgttg cgccggatac caaagctccg 1980 ggcctcaccc aggcgctaaa taccaaagat ggcgcagtga tggtgatgag ttacgggaac 2040 teegaagagg atteacaaga acatacegge agteagttge gtattgegge gtatggeeeg 2100 catgccgcca atgttgttgg actgaccgac cagaccgatc tcttctacac catgaaagcc 2160 gctctggggg atatcgcaca ccatcaccat caccattaa

<210> 90 <211> 732 <212> PRT <213> Artificial Sequence <220>

<223> Description of Artificial Sequence:198A2 scFv-alkaline phosphatase fusion protein (ORF of expression vector pDAP2-198AB2#100)

<400> 90

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala 10

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly 40 35

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr 70 75

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp 105 Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp 150 Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln 165 170 Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg 215 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu 250 245 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala 260 265 Ala Ala Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala 280 Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp 290 Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn 310 315 Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys 360 Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala 375 Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile 395

His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly 410 Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro 425 Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu 465 470 Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp 490 485 Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp 535 Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala 565 570 Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly 580 585 Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala 600 Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala 610 Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val 635 630 Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His 675 680 Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn 695 Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala 710 715

Ala Leu Gly Asp Ile Ala His His His His His 725 <210> 91 <211> 978 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:plasmid pZip-198AB2#102 <220> <221> modified base <222> (1)..(978) <223> n = g, a, c or t<400> 91 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60 atggcggagg tgaagctggt ggagtctggg ggaggcttag tgaagcctgg agggtccctg 120 aaactctcct gtgcagcctc tggattcact ttcagtagct ataccatgtc ttgggttcgc 180 cagacteegg agaagagget ggagtgggte gcaaccatta gtagtggngg tagtteeace 240 tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc 300 ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgtatta ctgtacaaga 360 gagggggtg gtttcaccgt caactggtac ttcgatgtct ggggcgcagg aacctcagtc 420 acceptetect caggtggagg eggtteaggt gggegegeet etggeggtgg eggateggae 480 attgtgctga cacaginico agoitettig goigtgtoio tagggcagag ggccaccata 540 tentgeagag ceagtgaaag tgttgatagt tatggetata attttatgea etggtateag 600 cagataccag gacagecace caaacteete atetategtg catecaacet agagtetggg 660 atccctgcca ggttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct 720 gtggaggctg atgatgttgc aacctattac tgtcagcaaa gtaatgagga tccgctcacg 780 ttcggtactg ggaccagact ggaaataaaa cgggcggccg caccgaagcc ttccactccg 840 cccgggtctt cccgtatgaa acagctggaa gacaaagtag aggagctcct tagcaagaac 900 taccatctag aaaacgaggt agctcgtctg aaaaagcttg ttggtgaacg tggtggtcac 960 catcaccatc accattaa <210> 92 <211> 325 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence:plasmid pZip-198AB2#102 <220> <221> MOD RES <222> (166) <223> Xaa = Cys, Tyr, Ser or Phe <400> 92 Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Ala

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly 20 25 30

5

10

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly 35 40

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu 50 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr 65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp 100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn 115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser 130 135 140

Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp 145 150 155 160

Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln 165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys 195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg 210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu 245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala 260 265 270

Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln 275 280 285

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu 290 295 300

Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His 305 310 315

His His His His 325

<210> 93

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mAB#8860
scFv-alkaline phosphatase fusion protein (vector construct pDAP2-8860scFv#11)

<400> 93 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60 atggccgagg ttcagcttca gcagtctgga cctgagctgg tgaagcccgg ggcctcagtg 120 aagattteet geaaagette tggetaegea tteagtaget ettggatgaa etgggtgaag 180 cagaggcctg gacagggtct tgagtggatt ggacggattt atcctggaaa tggagatact 240 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 300 gcctacatgc agctcagcag cctgacctct gtggactctg cggtctattt ctgtgcagat 360 ggtaacgtat attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 420 tcaggtggag gcggttcagg tgggcgcgcc tctggcggtg gcggatcgca aattgttctc 480 accoaqtoto otgottoott agotgtatot otggggcaga gggccaccat otcatgcagg 540 gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaacca 600 ggacagccac ccaaactcct catctatctt gcatccaacc tagaatctgg ggtccctgcc 660 aggttcagtg gcagtgggtc tgggacagac ttcaccctca acatccatcc tgtggaggag 720 gaggatgctg caacctatta ctgtcagcac agtagggagc ttcctcggac gttcggtgga 780 ggcaccaagc tggaaatcaa acgggcggcc gcagcccggg caccagaaat gcctgttctg 840 gaaaaccggg ctgctcaggg cgatattact gcacccggcg gtgctcgccg tttaacgggt 900 gatcagactg ccgctctgcg tgattctctt agcgataaac ctgcaaaaaa tattattttg 960 ctgattggcg atgggatggg ggactcggaa attactgccg cacgtaatta tgccgaaggt 1020 gegggegget tttttaaagg tatagatgee ttacegetta eegggeaata eacteactat 1080 gcgctgaata aaaaaaccgg caaaccggac tacgtcaccg actcggctgc atcagcaacc 1140 gcctggtcaa ccggtgtcaa aacctataac ggcgcgctgg gcgtcgatat tcacgaaaaa 1200 gatcacccaa cgattctgga aatggcaaaa gccgcaggtc tggcgaccgg taacgtttct 1260 accgcagagt tgcaggatgc cacgcccgct gcgctggtgg cacatgtgac ctcgcgcaaa 1320 tgctacggtc cgagcgcgac cagtgaaaaa tgtccgggta acgctctgga aaaaggcgga 1380 aaaggatcga ttaccgaaca gctgcttaac gctcgtgccg acgttacgct tggcggcggc 1440 gcaaaaacct ttgctgaaac ggcaaccgct ggtgaatggc agggaaaaac gctgcgtgaa 1500 caggcacagg cgcgtggtta tcagttggtg agcgatgctg cctcactgaa ttcggtgacg 1560 gaagegaate ageaaaaace eetgettgge etgtttgetg aeggeaatat geeagtgege 1620 tggctaggac cgaaagcaac gtaccatggc aatatcgata agcccgcagt cacctgtacg 1680 ccaaatccgc aacgtaatga cagtgtacca accctggcgc agatgaccga caaagccatt 1740 gaattgttga gtaaaaatga gaaaggcttt ttcctgcaag ttgaaggtgc gtcaatcgat 1800 aaacaggatc atgctgcgaa tccttgtggg caaattggcg agacggtcga tctcgatgaa 1860 gccgtacaac gggcgctgga attcgctaaa aaggagggta acacgctggt catagtcacc 1920 gctgatcacg cccacgccag ccagattgtt gcgccggata ccaaagctcc gggcctcacc 1980 caggogotaa ataccaaaga tggogoagtg atggtgatga gttacgggaa ctccgaagag 2040 gattcacaag aacataccgg cagtcagttg cgtattgcgg cgtatggccc gcatgccgcc 2100 aatgttgttg gactgaccga ccagaccgat ctcttctaca ccatgaaagc cgctctgggg 2160 2190 gatategeae accateacea teaceattaa

<210> 94 <211> 729 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB#8860 scFv-alkaline phosphatase fusion protein (vector construct pDAP2-8860scFv#11)

<400> 94

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala 1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu 20 25 30

. . . /

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly 40 Tyr Ala Phe Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys 90 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Ala Met 120 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly 130 135 Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr 185 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly 215 210 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu 230 235 Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ala 265 Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu 305 Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn 325 330 Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro 345

Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys 360 Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr 375 Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys 390 Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr 405 410 Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser 440 Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile 455 460 Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys 490 Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro 535 Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr 550 555 Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu 585 Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr 625 630 Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala 645 650 Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val 660 665

34 Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser 680 Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly 695 Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly 710 715 Asp Ile Ala His His His His His 725 <210> 95 <211> 969 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:mAB #8860 scFv-leucine zipper fusion protein (miniantibody vector construct p8860-Zip#1.2) <400> 95 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60 atggcggagg ttcagcttca gcagtctgga cctgagctgg tgaagcccgg ggcctcagtg 120 aaqatttcct gcaaagcttc tggctacgca ttcagtagct cttggatgaa ctgggtgaag 180 cagaggeetg gacagggtet tgagtggatt ggacggattt ateetggaaa tggagataet 240 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 300 gcctacatgc agctcagcag cctgacctct gtggactctg cggtctattt ctgtgcagat 360 gqtaacgtat attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 420 tcaggtggag gcggttcagg tgggcgcgcc tctggcggtg gcggatcgca aattgttctc 480 acccagtete etgetteett agetgtatet etggggeaga gggeeaceat eteatgeagg 540 gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaacca 600 ggacagccac ccaaactcct catctatctt gcatccaacc tagaatctgg ggtccctgcc 660 aggttcagtg gcagtgggtc tgggacagac ttcaccctca acatccatcc tgtggaggag 720 gaggatgctg caacctatta ctgtcagcac agtagggagc ttcctcggac gttcggtgga 780 ggcaccaagc tggaaatcaa acgggcggcc gcaccgaagc cttccactcc gcccgggtct 840 tcccgtatga aacagctgga agacaaagta gaggagctcc ttagcaagaa ctaccatcta 900 gaaaacgagg tagctcgtct gaaaaagctt gttggtgaac gtggtggtca ccatcaccat 960 caccattaa

<210> 96

<211> 322

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB #8860 scFv-leucine zipper fusion protein (miniantibody vector construct p8860-Zip#1.2)

<400> 96

Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Ala

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly 35 40 45

Tyr Ala Phe Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly 50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp 100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly 130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu 145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr 180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile 195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly 210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu 225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg 245 250 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Pro 260 265 270

Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp 275 280 285

Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val 290 295 300

Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His 305 310 315 320

His His

<210> 97

<211> 270

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:part of plasmid
      pMycHis6 differing from vector pCOCK
<400> 97
caggaaacag ctatgaccat gattacgcca agcttccatg aaaattctat ttcaaggaga 60
caqtcataat gaaataccta ttgcctacgg cagccgctgg attgttatta ctcgcggccc 120
agcoggocat ggoccaggtg cagotgcagg cgcgcctgca ggtcgacctc gagatcaaac 180
gggcggccgc agaacaaaaa ctcatctcag aagaggatct gaatggggcg gcacatcacc 240
atcaccatca ctaataagaa ttcactggcc
<210> 98
<211> 61
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:part of plasmid
      pMycHis6 differing from vector pCOCK
<400> 98
Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Ala
 1
                                     1.0
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val
Asp Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu
Glu Asp Leu Asn Gly Ala Ala His His His His His
     50
<210> 99
<211> 888
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:198AB2 scFv
      linked to c-myc-tag and His6 tag (ORF of
      expression vector pMycHis6-198AB2#102)
<220>
<221> modified base
<222> (228)
<223> n = g, a, c or t
<400> 99
atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60
atggccgagg tgaagctggt ggagtctggg ggaggcttag tgaagcctgg agggtccctg 120
aaacteteet gtgcageete tggatteact tteagtaget ataceatgte ttgggttege 180
cagacteegg agaagagget ggagtgggte geaaccatta gtagtggngg tagtteeace 240
tactatccag acagtgtgaa gggccgattc accatctcca gagacaatgc caagaacacc 300
ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgtatta ctgtacaaga 360
gagggggtg gtttcaccgt caactggtac ttcgatgtct ggggcgcagg aacctcagtc 420
acceptetect caggtggagg eggtteaggt gggegegeet etggeggtgg eggateggae 480
attgtgctga cacagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccata 540
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tcctgcagag ccagtgaaag tgttgatagt tatggctata attttatgca ctggtatcag 600

cagataccag gacagcacc caaactcctc atctatcgtg catccaacct agagtctggg 660 atccctgcca ggttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct 720 gtggaggctg atgatgttgc aacctattac tgtcagcaaa gtaatgagga tccgctcacg 780 ttcggtactg ggaccagact ggaaataaaa cgggcggccg cagaacaaaa actcatctca 840 gaagaggatc tgaatgggc ggcacatcac catcaccatc actaataa 888

<210> 100

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:198AB2 scFv linked to c-myc-tag and His6 tag (ORF of expression vector pMycHis6-198AB2#102)

<400> 100

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala 1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly 20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly 35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu 50 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr 65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp 100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn 115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser 130 135 140

Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp 145 150 155 160

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln 165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys 195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg 210 215 220 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro 235 225 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu 245 250 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala 280 His His His His His 290 <210> 101 <211> 876 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:mAB #8860 scFv linked to c-myc-tag and His6-tag designated 8860-M/H#4c (plasmid vector p8860-M/H#4c) atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60 atggccgagg ttcagcttca gcagtctgga cctgagctgg tgaagcccgg ggcctcagtg 120 aagattteet geaaagette tggetaegea tteagtaget ettggatgaa etgggtgaag 180 cagaggcctg gacagggtct tgagtggatt ggacggattt atcctggaaa tggagatact 240 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 300 gcctacatgc agctcagcag cctgacctct gtggactctg cggtctattt ctgtgcagat 360 qqtaacqtat attactatqc tatggactac tggggtcaag gaacctcagt caccgtctcc 420 tcaggtggag gcggttcagg tgggcgcgcc tctggcggtg gcggatcgca aattgttctc 480 accoagtote etgetteett agetgtatet etggggeaga gggecaceat eteatgeagg 540 gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaacca 600 ggacagccac ccaaactcct catctatctt gcatccaacc tagaatctgg ggtccctgcc 660 aggttcagtg gcagtgggtc tgggacagac ttcaccctca acatccatcc tgtggaggag 720 gaggatgctg caacctatta ctgtcagcac agtagggagc ttcctcggac gttcggtgga 780 qqcaccaaqc tqqaaatcaa acgggcggcc gcagaacaaa aactcatctc agaagaggat 840 ctgaatgggg cggcacatca ccatcaccat cactaa <210> 102 <211> 291 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence:mAB #8860 scFv linked to c-myc-tag and His6-tag designated 8860-M/H#4c (plasmid vector p8860-M/H#4c) <400> 102 Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Ala

1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly 35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly 50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp 100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Ala Met 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly 130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu 145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr 165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile 195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly 210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu 225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg 245 250 255

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Glu 260 265 270

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His 275 280 285

His His His 290

<210> 103

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

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<400> 103
ggccgcagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca 60
ccatcactaa taag
<210> 104
<211> 69
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:annealed
      oligonucleotide
<400> 104
ttattagtga tggtgatggt gatgtgccgc cccattcaga tcctcttctg agatgagttt 60
ttgttctgc
<210> 105
<211> 16
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:CDR3 peptide
<220>
<221> MOD_RES
<222> (1)..(16)
<223> Xaa = any amino acid
<400> 105
Cys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys
<210> 106
<211> 16
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: CDR3 peptide
<400> 106
Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp
                                                          15
                                     10
 1
<210> 107
<211> 30
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:portion of
      plasmid pMycHis6 with pelB-leader, polylinker and
      c-myc tag
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<400> 107

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Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu
Gln Val Asp Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys
<210> 108
<211> 90
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:portion of
      plasmid pMycHis6 with pelB-leader, polylinker and
      c-myc tag
<400> 108
ctegeggece ageeggeeat ggeeeaggtg eagetgeagg egegeetgea ggtegaeete 60
gagatcaaac gggcggccgc agaacaaaaa
<210> 109
<211> 12
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:c-myc-tag
<400> 109
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly
<210> 110
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: His6-tag
<400> 110
His His His His His
 1
                 5
<210> 111
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: flexible linker
Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser
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<210> 112
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Al peptide core sequence

<400> 112
Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp
1 5 10